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Biogeosciences Discussions

Interactive comment on "Crustal uplifting rate associated with late-Holocene glacial-isostatic rebound at Skallen and Skarvsnes, Lützow-Holm Bay, East Antarctica: evidence of a synchrony in sedimentary and biological facies on geological setting" *by* Y. Takano et al.

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First of all, we thank the referee for the constructive reviews (Biogeosciences Discuss., 7, C2429–C2430, 2010: www.biogeosciences-discuss.net/7/C2429/2010/). We sincerely appreciate the comment which helped us to improve this manuscript.

Please find our responses to the general and specific comments below.

Specific comments: (1) The manuscript tried to reconstruct the isostatic rebound history of the studied area, and is well organized in terms of its geological and geochemical descriptions. However, I greatly doubt about the applicability of 16S rRNA-based DGGE profiling to increase the accuracy of the reconstructed geo-history. First, the DNA signatures in the sediments are of modern-living organisms that may not necessarily reflect the changes in the past. In the case of ancient DNA studies, genetic materials are extracted from geologically "fixed" samples such as ice cores, permafrost, amber, salt rock halite, etc. Shallow sediments are not regarded as such.

[Reply] Of course, we need careful interpretations in terms of ancient DNA/RNA signals. However, in the present study, the distinct laminations in the core sediment (Figure 3) indicates each past organism accumulated in the geological time scale (see also, the radio-carbon age determination in Figure 4). Therefore, we concluded that the ancient molecular signals were “fixed” in the laminated (varved) sequences.

(2) Second, if diatoms were to be targeted, 18S-rRNA based, not 16S based, characterization should be done. Should the extracted bulk DNA samples be still available, then it looks very easy to do the work. There are diatom-targeted PCR primers published.

[Reply] We agree with the comment that this would be bullet-proof evidence for the proposed analysis. Although the suggested experiments can only be conducted as part of new study with independent procedural design, it is notable that the retrieved sequences from the DGGE bands were closely related to 16S rDNA from the chloroplast of the marine diatom. We are currently submitting a proposal for conducting this fossil diatom assemblage with 16S rRNA analysis.

(3) Third, the DGGE is not a best way to characterize microbial communities of the past or modern. It is well known that DGGE profiles are variable due to the DNA extraction methods, quality of extracted DNA, and PCR conditions including primers. Moreover, even the DGGE bands at the same position may result in different sequences. For this

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reason, some laboratories including my lab perform "all bands sequencing" for every DGGE occasion, though we are not usually inclined to DGGE. For the reasons stated above, I would conclude that DGGE decreases or damage greatly the accuracy of the proposed geo-history. In other words, the ms without DGGE will be more informative.

[Reply] We already replied the discussion of past or modern signal from the insight of radio-carbon age. We think that DGGE is an efficient and clear-cut pre-treatment to purify the molecular signals from sediment samples. As to quality control of our DGGE procedures, we previously conducted by using Antarctica samples (Fujii et al., 2010). Consequently, we believe that the ancient phototroph community members have been confirmed based on comparative sequence analyses including DGGE.

Fujii, M., Takano, Y., Kojima, H., Hoshino, T., Tanaka, R., Fukui, M., (2010) Microbial community structure, pigment composition, and nitrogen source of red snow in Antarctica. Microbial Ecology, 59, 466–475.

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Interactive comment on Biogeosciences Discuss., 7, 4341, 2010.